

SEQUENCE LISTING

<110> Agriculture and Agri-Food Canada; The University of Saskatchewan

<120> Cyclin Dependant Kinase Inhibitors as Plant Growth
Regulators

<130> 81601-3

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<150> CA 2,256,121

<151> 1998-12-31

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 904

<212> DNA

<213> Arabidopsis thaliana

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tca acg tat atg cag cta cgg agc cgg aga att gtt tat gtt aga tcg      153
Ser Thr Tyr Met Gln Leu Arg Ser Arg Arg Ile Val Tyr Val Arg Ser
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gaa aaa tca agc tct gtc tcc gtc gtc ggt gat aat gga gtt tcg tcg      201
Glu Lys Ser Ser Ser Val Ser Val Val Gly Asp Asn Gly Val Ser Ser
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tct tgt agt gga agc aat gaa tat aag aag aaa gaa tta ata cat ctg      249
Ser Cys Ser Gly Ser Asn Glu Tyr Lys Lys Lys Glu Leu Ile His Leu
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gtg acg aag agg aag ctt ttt gaa aat ctg aga gag gag gag aaa gaa 345
 Val Thr Lys Arg Lys Leu Phe Glu Asn Leu Arg Glu Glu Glu Lys Glu
 85 90 95

gaa tta agt aaa tcc atg gag aat tat tca tcg gaa ttt gaa tcg gcg 393
 Glu Leu Ser Lys Ser Met Glu Asn Tyr Ser Ser Glu Phe Glu Ser Ala
 100 105 110

gtt aaa gaa tcg tta gat tgt tgt tgt agc ggg agg aaa acg atg gag 441
 Val Lys Glu Ser Leu Asp Cys Cys Cys Ser Gly Arg Lys Thr Met Glu
 115 120 125

gag acg gtg acg gcg gag gag gag gag aag gcg aaa ttg atg acg gag 489
 Glu Thr Val Thr Ala Glu Glu Glu Glu Lys Ala Lys Leu Met Thr Glu
 130 135 140 145

atg cca acg gaa tcg gaa att gaa gat ttt ttt gtg gaa gct gag aaa 537
 Met Pro Thr Glu Ser Glu Ile Glu Asp Phe Phe Val Glu Ala Glu Lys
 150 155 160

caa ctc aaa gaa aaa ttc aag aag aag tac aat ttc gat ttc gag aag 585
 Gln Leu Lys Glu Lys Phe Lys Lys Lys Tyr Asn Phe Asp Phe Glu Lys
 165 170 175

gag aag cca tta gaa gga cgt tac gaa tgg gta aag tta gag 627
 Glu Lys Pro Leu Glu Gly Arg Tyr Glu Trp Val Lys Leu Glu
 180 185 190

tgaagaagaa gaagaagttt atggtttttt ttttaacttt ttagatttta atatttcagg 687

gaataagtta attttatttt gttgatttgg aaatataaga tttgtaggag gaatgttttt 747

agaagtacga aattgcacag aaaaagaaga aagcttttta acagatttta gagcccagaa 807

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 35 40 45

Ser Ser Cys Ser Gly Ser Asn Glu Tyr Lys Lys Lys Glu Leu Ile His
 50 55 60

Leu Glu Glu Glu Asp Lys Asp Gly Asp Thr Glu Thr Ser Thr Tyr Arg
 65 70 75 80
 Arg Val Thr Lys Arg Lys Leu Phe Glu Asn Leu Arg Glu Glu Glu Lys
 85 90 95
 Glu Glu Leu Ser Lys Ser Met Glu Asn Tyr Ser Ser Glu Phe Glu Ser
 100 105 110
 Ala Val Lys Glu Ser Leu Asp Cys Cys Cys Ser Gly Arg Lys Thr Met
 115 120 125
 Glu Glu Thr Val Thr Ala Glu Glu Glu Lys Ala Lys Leu Met Thr
 130 135 140
 Glu Met Pro Thr Glu Ser Glu Ile Glu Asp Phe Phe Val Glu Ala Glu
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 aagccattag aaggacgtta cgaatgggta aagttagagt gaagaagaag aagaagttta 540
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 ggaggagaag gcgaaattga tgacggagat gccaacggaa tcggaaattg aagatttttt 240
 tgtggaagct gagaaacaac tcaaagaaaa attcaagaag aagtacaatt tcgatttcga 300
 gaaggagaag ccattagaag gacgttacga atgggtaaag ttagagtga gaagaagaag 360
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 gtagattgt tggtgtagcg ggaggaaaac gatggaggag gaggaggaga aggcgaaatt 180
 gatgacggag atgccaacgg aatcggaat tgaagatttt tttgtggaag ctgagaaaca 240
 actcaaagaa aaattcaaga agaagtacaa tttcgatttc gagaaggaga agccattaga 300
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 cctccggttg aagaacagtg tcaaatecga gaagaagatt cgtcggtttc gtgttgttct 180
 acatcggaag agaaatcgaa acggagaatc gaattttag atcttgagga aaataacggt 240
 gacgatcgtg aaacagaaac gtcgtggatt tacgatgatt tgaataagag tgaggaatcg 300
 atgaacatgg attcttcttc ggtggctgtt gaagatgtag agtctcgccg caggttaagg 360
 aagagtctcc atgagacggt gaaggaagct gagttagaag acttttttca ggtggcggag 420
 aaagatcttc ggaataagtt gttggaatgt tctatgaagt ataacttcga tttcgagaaa 480
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65 70 75 80

Ser Ser Ile Ser Ser Gly Cys Ser Ser Ser Glu Thr Asn Glu Ile Ala
85 90 95

Thr Arg Leu Pro Phe Ser Asp Leu Glu Ala His Glu Ile Ser Glu Thr
100 105 110

Glu Ile Ser Thr Leu Leu Thr Asn Asn Phe Arg Lys Gln Gly Ile Ser
115 120 125

Ser Ser Glu Asn Leu Gly Glu Thr Ala Glu Met Asp Ser Ala Thr Thr
130 135 140

Glu Met Arg Asp Gln Arg Lys Thr Glu Lys Lys Lys Lys Met Glu Lys
145 150 155 160

Ser Pro Thr Gln Ala Glu Leu Asp Asp Asp Phe Phe Ser Ala Ala Glu
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35 40 45

His Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe Val Glu Asp Met Glu
50 55 60

Ile Met Val Thr Pro Gly Ser Ser Thr Arg Ser Met Cys Arg Ala Thr
65 70 75 80

Lys Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile Pro Thr Thr Ser Glu
85 90 95

Leu Glu Val Ala Ala Val Val Glu Glu Glu Glu Val Ala Asn Cys Ser
 50 55 60
 Ser Ser Glu Val Ile Thr Thr Ala Arg Ser Asp Phe Pro Pro Ser Cys
 65 70 75 80
 Cys Ser Ser Asn Tyr Asp Gln Leu Ser Ser Ser Glu Pro Glu Val Val
 85 90 95
 Lys Asp Asp Asp Gly Leu Gly Asn Arg Thr Ala Asp Pro Glu Val Glu
 100 105 110
 Ser Gly Glu Ala Ser Ser Lys Gln Lys Glu Ser His Arg Thr Glu Ala
 115 120 125
 Arg Glu Ala Thr Lys Leu Asp Asp Gln Asp Tyr Pro Ala Thr Lys Ser
 130 135 140
 Thr Val Gln Ile Lys Met Pro Ser Asp Ser Glu Ile Glu Glu Phe Phe
 145 150 155 160
 Ala Val Ala Glu Lys Asp Leu Gln Lys Arg Phe Ser Glu Lys Tyr Asn
 165 170 175
 Phe Asp Ile Val Lys Asp Val Pro Leu Lys Gly Arg Tyr Asp Trp Val
 180 185 190
 Pro Ile Asn Pro
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